

**Figure 1.**

```
1 mdvtiqhpwf krtlgpfyps rlfdqffgeg lfeydlpfl sstispyyrq slfrtvldsg
61 iseversdrdk fvifldvkhf spedltvkvg ddfveihgkh nerqddhgyi srefhrryrl
121 psnvdsals csldsagmlt fcgpkigtgl dathaeraip vsreekptsa pss
```

**Figure 2.**

```
1 tccctcttcc gcaccgtgct ggactccggc atctctgagg ttcgatccga cggggacaag
61 ttcgtcatct tcctcgatgt gaagcacttc tccccggagg acctcaccgt gaagggtgcag
121 gacgactttg tggagatcca cggaaagcac aacgagcgcc aggacgacca cggctacatt
181 tcccgtagt tccaccgcc ctaccgctg ccgtccaacg tggaccagtc ggccctctct
241 tgctccctgt ctgccgatgg catgctgacc ttctgtggcc ccaagatcca gactggcctg
301 gatgccaccc acgccgagcg agccatcccc gtgtcgcggg aggagaagcc cacctcggct
361 cctcgtcct aa
```

**Figure 3.**

```
1 slfrtvldsg iseversdrdk fvifldvkhf spedltvkvg ddfveihgkh nerqddhgyi
61 srefhrryrl psnvdsals csldsagmlt fcgpkigtgl dathaeraip vsreekptsa
121 pss
```

2495337  
hs12\_caeel\_2  
hs11\_orysa\_1  
hs11\_pea\_1  
SP21\_STIAU  
hs27\_mouse\_3  
craa\_bovin\_1  
crab\_bovin\_1  
cra2\_mouse\_1

```
mford.....pfds1fermfkeffatpmtgttmi0sst.....
MSL.....YHYFRPAQORSVFGLMRDMALM.....
MSLV.....RR.....SNVFD.PFSLDLWDPF.DSVFRSVV.....
MSLI...PSFFSGRR.....SNVFD.PFSLDVWDPLKDFPFSS.....
MADLSV.....RRCTGST.....PORTREWD.PFOOMOELMNW.DPFEIAN.....
MTERRV..PFSLLRSPSWEPFRDWYPAHSRLFDQAFGVRLPDEW.SQWFSAACWPKYVR
MDIAIQH.PWF..KRTLG...PFY..PSRLFDOFFEGELFEYDIL.PFLSSTISPYIRO
MDIAIHH.PWI..RRPFF...PFH.SPSRLFDOFFEGEHLLESDF..PASTSLSPFYLR
MDVTIOH.PWF..KRALG...PFY..PSRLFDOFFEGELFEYDIL.PFLSSTISPYIRO
```

2495337  
hs12\_caeel\_2  
hs11\_orysa\_1  
hs11\_pea\_1  
SP21\_STIAU  
hs27\_mouse\_3  
craa\_bovin\_1  
crab\_bovin\_1  
cra2\_mouse\_1

```
.....gigisqkg...fmpisiie.....
.....ERQFAPVCRIS...PSESSEIV.....
.....PATSDNDT.AAFANARIDW.....K
.....PSASFPRENPAFVSTRVDW.....K
.....HPWFANROCP.PAFVPAFEV.....R
PLPAATAEGPAAVTLAA.PAFSRALNROLSSGVSEI.....R
.....SLFRTV...LDSGISEV.....R
.....PPSFLRAPSW.IDTGLSEM.....R
.....SLFRTV...LDSGISELMTHMWFVNMHOPHAGNPKNNPVKVR
```

2495337  
hs12\_caeel\_2  
hs11\_orysa\_1  
hs11\_pea\_1  
SP21\_STIAU  
hs27\_mouse\_3  
craa\_bovin\_1  
crab\_bovin\_1  
cra2\_mouse\_1

```
dgghikvialwl..pgvknkediilnavgd.tleirakrsplmitesser.iilyseipeeeeliy
NNDOKFAINLNVSOFKPEDLKINLDCR.TLSIOGEOELKT.....DHGYSKK...SFS
ETPESHVFKADLPGVKKEEVKVEVEECNVLVISGORSKEKEDKNDKWHERVERSS..GQFM
ETPEAHVFKADLPGLKKEEVKVEVEDDRVLOISGERSVEKEDKNDKWHERVERSS..GKFL
ETKEAYIFKADLPGVDEKDIEVTLTCD.RVSVSGKREKREKREESERFYAYERTF..CSFS
QTADRWRVSLDVNHFAPPEELTVKTKEG.VVEITGKHEERO.....DEHGYISR...CFT
SDRDKFVIFLDVKHFSPEDLTVKVOED.FVEIHGKHNERO.....DDHGYISR...EFF
LEKDRFSVNLDVKHFSPEELKVKVLCD.VIEVHGKHEERO.....DEHGFISR...EFF
SDRDKFVIFLDVKHFSPEDLTVKVLED.FVEIHGKHNERO.....DDHGYISR...EFF
```

2495337  
hs12\_caeel\_2  
hs11\_orysa\_1  
hs11\_pea\_1  
SP21\_STIAU  
hs27\_mouse\_3  
craa\_bovin\_1  
crab\_bovin\_1  
cra2\_mouse\_1

```
rtiklpatvke.enasakfengvlsvilpkaessi.kk.ginie.~~~~~.~~~~~
RVILIPEDVDVGAVASNLSEDGKLSIEAPKKEAVOGRSIPIOQAIV..EEKSAE~~~~~
RRFRLPENAKV.DQVKAQLENGVLTVTVPKAEV...KK.PEVKAI...EISC.....
RRFRLPENAKM.DKVKASMENGVLTVTPKEEI...KK.AEVKSI...EISC.....
RAFTLPEGVDG.DNVRADLKNGVLTTLTPKRPEV.OPK.RIOVASSQTEOKEIKAYPAP
RKYTLPPGVDPPTLVSSSLSPECTLTVEAPLPKAV..TQSAEITIPVTFEARAQIGQPEAC
RRYRLPSNVDSALSCSLSADGMLTFSGPKIPSGVDAGHSERAI PVSREEKPSSAPSS~~
RKYRIPADVDP LAITSSLSSDGVLTVNGPRKO...ASC PERTIPITREEKPAVTAAP..
RRYRLPSNVDSALSCSLSADGMLTFSGPKVOSGLDAGHSERAI PVSREEKPSSAPSS~~
```

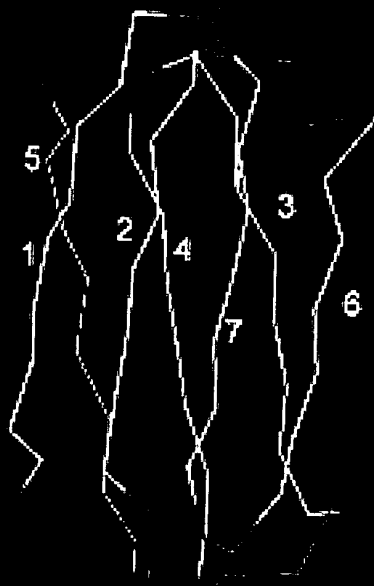
2495337  
hs12\_caeel\_2  
hs11\_orysa\_1  
hs11\_pea\_1  
SP21\_STIAU  
hs27\_mouse\_3  
craa\_bovin\_1  
crab\_bovin\_1  
cra2\_mouse\_1

```
~~~~~
~~~~~
.....~~~~~
.....~~~~~
AEPGLAAPLQWPGFS~~~~~
KSEOSQAK~~~~~
~~~~~
.KK~~~~~
~~~~~
```

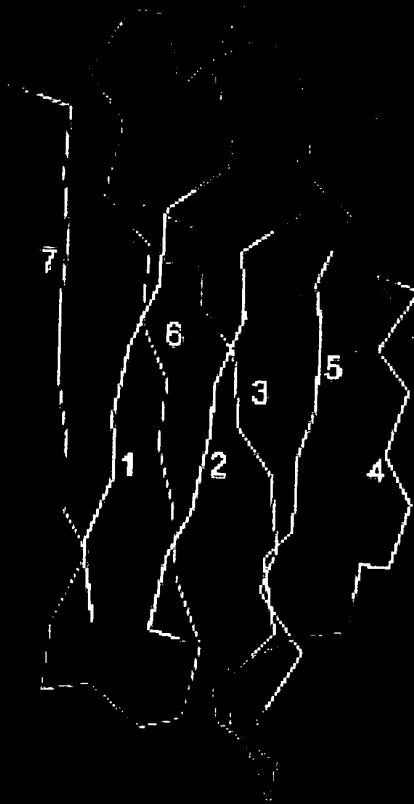
Figure s 4A and 4B

```
HSP16 ( A33)  G I I S G K - G F M - - P I S I I (A49)
CRAA_B ( 45) S P Y Y R C E L F R T V L D S G - - I E V R S (66)
          | | | | | | | | | | | | | | | | | | | | | |
HSP16 ( gap ) - G D Q I I K V I A M L P G V N K E - - I I L (A70)
CRAA_B ( gap ) - D R D K F V I F L D V K H F S P E - - D L V (87)
          | | | | | | | | | | | | | | | | | | | | | |
HSP16 ( A71) N A V - - G D T L E I R A K R S P L M I T E S E (A92)
CRAA_B ( 88) K V Q - - E D F V E I H G K H N E R Q - - - - D (105)
          | | | | | | | | | | | | | | | | | | | | | |
HSP16 ( A93) R I I Y S E I P E E E E I Y R I K L P A T V K (A116)
CRAA_B ( 106) D H G Y I - - - - S R E F H R R Y R L P S N V D (125)
          | | | | | | | | | | | | | | | | | | | | | |
HSP16 ( A117) E E N A S A F - E N G V L S V I L P K A E S S (A139)
CRAA_B ( 126) Q S A L S C S L S A D G M L T F S G P K I P S G (149)
          | | | | | | | | | | | | | | | | | | | | | |
```

Figure 5



**HSP16**



**FCC**

**Figure 6**



Figur 7A

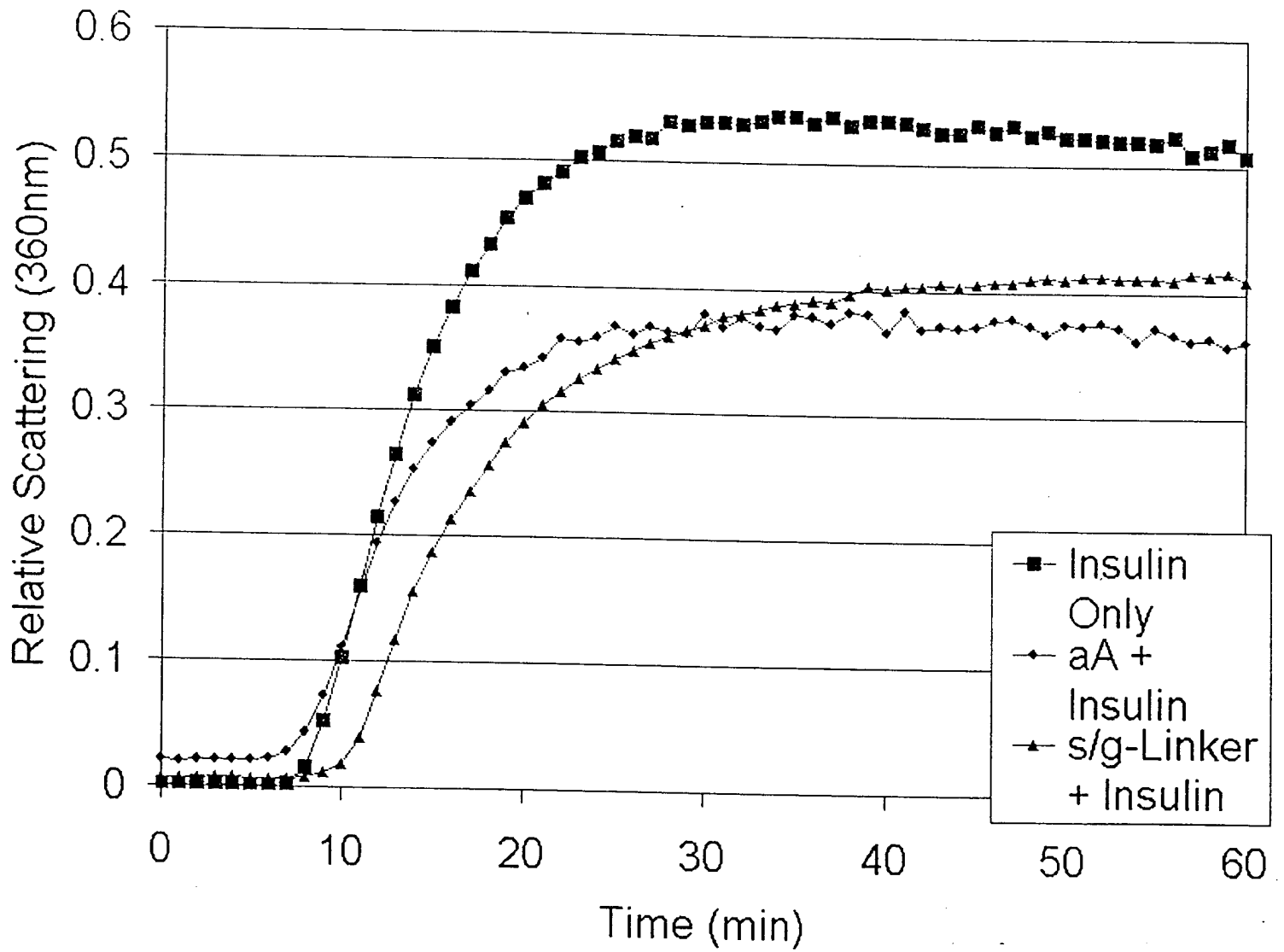
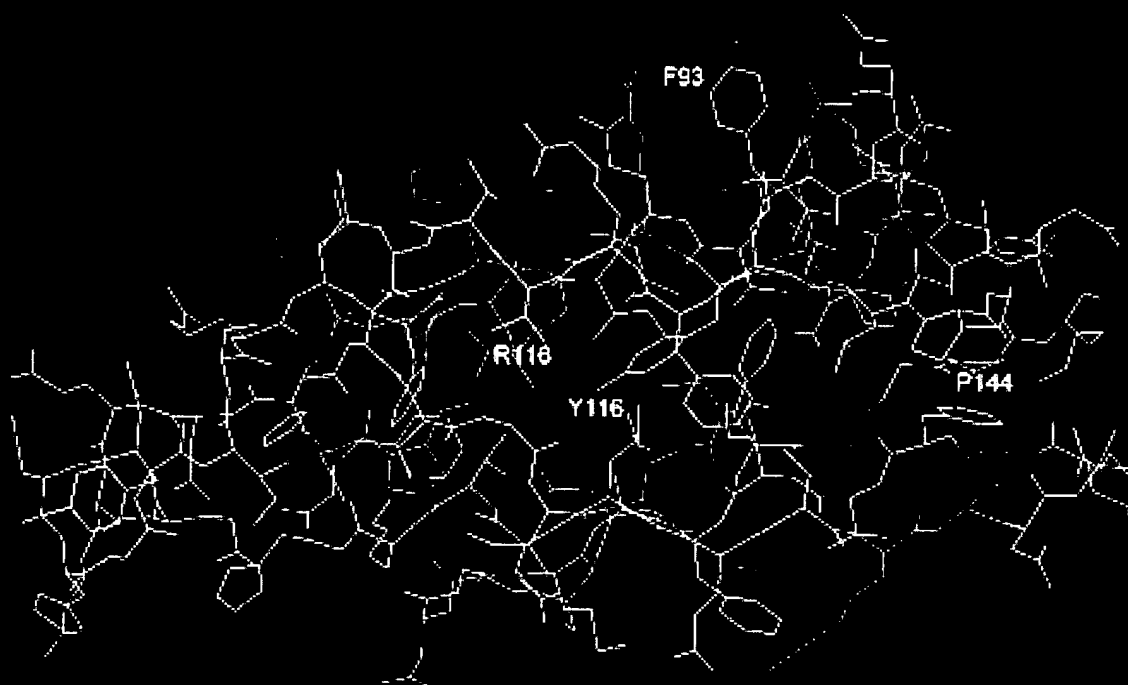


Figure 8



**Figure 7B**